Figure 1

1 GAGAGAAGGA GAAGATAATA TACTGAAAAG AAGAGGAGGA GGAGAGCGAC GGGACGGGAC
61 GCGAGCGGGA GCGCAGCCGC CCTCTCGGCT CCGCGGCGGC GCCTCGCAAG TCCGGGAGGC
121 GAGGGGGGCC CGAGGGGAGA CGCCGTGACA ACTTTCGTTT CCCTCTGAGG GAATTGGGAG
181 GTCGGCGGCC CCAAAAGCTT TCAGTCCAGT GTAAAGCTGT TGGAGCGCGG GAGCAAAGGT
241 AAAGAATGAT GTAATGCGCT GGCTGCTCCA AAGCATCTTT TGTTGTGGAA TGGTTATTCC
301 AGTCATCTCT TTATGAATCA AATGTGAGGG GCTGCTTTGT GGACGGAGTC CTTTGCAAGA
361 GCACATCAAC GGGAAAGAGA AAGAGACATT CACTTGGAGG GCTCTTGCTG AAAATGGGTT
421 TAACTCTCCT TTTGCCAGTC ACCACCAGCC TGACCTCATA CACTTTTAGT ACAATGGAGT
481 GGCTGAGCCT TTGAGCACAC CACCATTACA TCATCGTGGC AAATTAAAGA AGGAGGTGGG
541 AAAAGAGGAC TTATTGTTGT C**ATG**GCCCAT GAGATGATTG GAACTCAAAT TGTTACTGAG
601 AGGTTGGTGG CTCTGCTGGA AAGTGGAACG GAAAAAGTGC TGCTAATTGA TAGCCGGCCA
661 TTTGTGGAAT ACAATACATC CCACATTTTG GAAGCCATTA ATATCAACTG CTCCAAGCTT
721 ATGAAGCGAA GGTTGCAACA GGACAAAGTG TTAATTACAG AGCTCATCCA GCATTCAGCG
781 AAACATAAGG TTGACATTGA TTGCAGTCAG AAGGTTGTAG TTTACGATCA AAGCTCCCAA
841 GATGTTGCCT CTCTCTCTTC AGACTGTTTT CTCACTGTAC TTCTGGGTAA ACTGGAGAAG
901 AGCTTCAACT CTGTTCACCT GCTTGCAGGT GGGTTTGCTG AGTTCTCTCG TTGTTTCCCT
961 GGCCTCTGTG AAGGAAAATC CACTCTAGTC CCTACCTGCA TTTCTCAGCC TTGCTTACCT
1021 GTTGCCAACA TTGGGCCAAC CCGAATTCTT CCCAATCTTT ATCTTGGCTG CCAGCGAGAT
1081 GTCCTCAACA AGGAGCTGAT GCAGCAGAAT GGGATTGGTT ATGTGTTAAA TGCCAGCAAT
1141 ACCTGTCCAA AGCCTGACTT TATCCCCGAG TCTCATTTCC TGCGTGTGCC TGTGAATGAC
1201 AGCTTTTGTG AGAAAATTTT GCCGTGGTTG GACAAATCAG TAGATTTCAT TGAGAAAGCA
1261 AAAGCCTCCA ATGGATGTGT TCTAGTGCAC TGTTTAGCTG GGATCTCCCG CTCCGCCACC
1321 ATCGCTATCG CCTACATCAT GAAGAGGATG GACATGTCTT TAGATGAAGC TTACAGATTT
1381 GTGAAAGAAA AAAGACCTAC TATATCTCCA AACTTCAATT TTCTGGGCCA ACTCCTGGAC
1441 TATGAGAAGA AGATTAAGAA CCAGACTGGA GCATCAGGGC CAAAGAGCAA ACTCAAGCTG
1501 CTGCACCTGG AGAAGCCAAA TGAACCTGTC CCTGCTGTCT CAGAGGGTGG ACAGAAAAGC
1561 GAGACGCCCC TCAGTCCACC CTGTGCCGAC TCTGCTACCT CAGAGGCAGC AGGACAAAGG
1621 CCCGTGCATC CCGCCAGCGT GCCCAGCGTG CCCAGCGTGC AGCCGTCGCT GTTAGAGGAC
1681 AGCCCGCTGG TACAGGCGCT CAGTGGGCTG CACCTGTCCG CAGACAGGCT GGAAGACAGC
1741 AATAAGCTCA AGCGTTCCTT CTCTCTGGAT ATCAAATCAG TTTCATATTC AGCCAGCATG
1801 GCAGCATCCT TACATGGCTT CTCCTCATCA GAAGATGCTT TGGAATACTA CAAACCTTCC
1861 ACTACTCTGG ATGGGACCAA CAAGCTATGC CAGTTCTCCC CTGTTCAGGA ACTATCGGAG
1921 CAGACTCCCG AAACCAGTCC TGATAAGGAG GAAGCCAGCA TCCCCAAGAA GCTGCAGACC
1981 GCCAGGCCTT CAGACAGCCA GAGCAAGCGA TTGCATTCGG TCAGAACCAG CAGCAGTGGC
2041 ACCGCCCAGA GGTCCCTTTT ATCTCCACTG CATCGAAGTG GGAGCGTGGA GGACAATTAC
2101 CACACCAGCT TCCTTTTCGG CCTTTCCACC AGCCAGCAGC ACCTCACGAA GTCTGCTGGC
2161 CTGGGCCTTA AGGGCTGGCA CTCGGATATC TTGGCCCCCC AGACCTCTAC CCCTTCCCTG
2221 ACCAGCAGCT GGTATTTTGC CACAGAGTCC TCACACTTCT ACTCTGCCTC AGCCATCTAC
2281 GGAGGCAGTG CCAGTTACTC TGCCTACAGC TGCAGCCAGC TGCCCACTTG CGGAGACCAA
2341 GTCTATTCTG TGCGCAGGCG GCAGAAGCCA AGTGACAGAG CTGACTCGCG GCGGAGCTGG
2401 CATGAAGAGA GCCCCTTTGA AAAGCAGTTT AAACGCAGAA GCTGCCAAAT GGAATTTGGA
2461 GAGAGCATCA TGTCAGAGAA CAGGTCACGG GAAGAGCTGG GGAAAGTGGG CAGTCAGTCT
2521 AGCTTTTCGG GCAGCATGGA AATCATTGAG GTCTCC**TGA**G AAGAAAGACA CTTGTGACTT
2581 CTATAGACAA TTTTTTTTTC TTGTTCACAA AAAAATTCCC TGTAAATCTG AAATATATAT
2641 ATGTACATAC ATATATATTT TTGGAAAATG GAGCTATGGT GTAAAAGCAA CAGGTGGATC
2701 AACCCAGTTG TTACTCTCTT AACATCTGCA TTTGAGAGAT CAGCTAATAC TTCTCTCAAC
2761 AAAAATGGAA GGGCAGATGC TAGAATCCCC CCTAGACGGA GGAAAACCAT TTTATTCAGT
2821 GAATTACACA TCCTCTTGTT CTTAAAAAAG CAAGTGTCTT TGGTGTTGGA GGACAAAATC
2881 CCCTACCATT TTCCACGTTG TGCTACTAAG AGATCTCAAA TATTAGTCTT TGTCCGGACC
2941 CTTCCATAGT ACACCTTAGC GCTGAGACTG AGCCAGCTTG GGGGTCAGGT AGGTAGACCC
3001 TGTTAGGGAC AGAGCCTAGT GGTAAATCCA AGAGAAATGA TCCTATCCAA AGCTGATTCA
3061 CAAACCCACG CTCACCTGAC AGCCGAGGGA CACGAGCATC ACTCTGCTGG ACGGACCATT
3121 AGGGGCCTTG CCAAGGTCTA CCTTAGAGCA AACCCAGTAC CTCAGACAGG AAAGTCGGGG
3181 CTTTGACCAC TACCATATCT GGTAGCCCAT TTTCTAGGCA TTGTGAATAG GTAGGTAGCT
3241 AGTCACACTT TTCAGACCAA TTCAAACTGT CTATGCACAA AATTCCCGTG GGCCTAGATG
3301 GAGATAATTT TTTTTTCTTC TCAGCTTTAT GAAGAGAAGG GAAACTGTCT AGGATTCAGC
3361 TGAACCACCA GGAACCTGGC AACATCACGA TTTAAGCTAA GGTTGGGAGG CTAACGAGTC
3421 TACCTCCCTC TTTGTAAATC AAAGAATTGT TTAAAATGGG ATTGTCAATC CTTTAAATAA
3481 AGATGAACTT GGTTTC

Figure 2.

MAHEMIGTQIVTERLVALLESGTEKVLLIDSRPFVEYNTSHILEAININCSKLMKRRLQQDKVLITELIQHSAKHKV
DIDCSQKVVVYDQSSQDVASLSSDCFLTVLLGKLEKSFNSVHLLAGGFAEFSRCFPGLCEGKSTLVPTCISQPCLPV
ANIGPTRILPNLYLGCQRDVLNKELMQQNGIGYVLNASNTCPKPDFIPESHFLRVPVNDSFCEKILPWLDKSVDFIE
KAKASNGCVLVHCLAGISRSATIAIAYIMKRMDMSLDEAYRFVKEKRPTISPNFNFLGQLLDYEKKIKNQTGASGPK
SKLKLLHLEKPNEPVPAVSEGGQKSETPLSPPCADSATSEAAGQRPVHPASVPSVPSVQPSLLEDSPLVQALSGLHL
SADRLEDSNKLKRSFSLDIKSVSYSASMAASLHGFSSSEDALEYYKPSTTLDGTNKLCQFSPVQELSEQTPETSPDK
EEASIPKKLQTARPSDSQSKRLHSVRTSSSGTAQRSLLSPLHRSGSVEDNYHTSFLFGLSTSQQHLTKSAGLGLKGW
HSDILAPQTSTPSLTSSWYFATESSHFYSASAIYGGSASYSAYSCSQLPTCGDQVYSVRRRQKPSDRADSRRSWHEE
SPFEKQFKRRSCQMEFGESIMSENRSREELGKVGSQSSFSGSMEIIEVS

Figure 3.

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   1 GAGAGAAGGA GAAGATAATA TACTGAAAAG AAGAGGAGGA GGAGAGCGAC GGGACGGGAC
  61 GCGAGCGGGA GCGCAGCCGC CCTCTCGGCT CCGCGGCGGC GCCTCGCAAG TCCGGGAGGC
 121 GAGGGGGGCC CGAGGGGAGA CGCCGTGACA ACTTTCGTTT CCCTCTGAGG GAATTGGGAG
 181 GTCGGCGGCC CCAAAAGCTT TCAGTCCAGT GTAAAGCTGT TGGAGCGCGG GAGCAAAGGT
 241 AAAGAATGAT GTAATGCGCT GGCTGCTCCA AAGCATCTTT TGTTGTGGAA TGGTTATTCC
 301 AGTCATCTCT TTATGAATCA AATGTGAGGG GCTGCTTTGT GGACGGAGTC CTTTGCAAGA
 361 GCACATCAAC GGGAAAGAGA AAGAGACATT CACTTGGAGG GCTCTTGCTG AAAATGGGTT
 421 TAACTCTCCT TTTGCCAGTC ACCACCAGCC TGACCTCATA CACTTTTAGT ACAATGGAGT
 481 GGCTGAGCCT TTGAGCACAC CACCATTACA TCATCGTGGC AAATTAAAGA AGGAGGTGGG
 541 AAAAGAGGAC TTATTGTTGT CATGGCCCAT GAGATGATTG GAACTCAAAT TGTTACTGAG
 601 AGGTTGGTGG CTCTGCTGGA AAGTGGAACG GAAAAAGTGC TGCTAATTGA TAGCCGGCCA
 661 TTTGTGGAAT ACAATACATC CCACATTTTG GAAGCCATTA ATATCAACTG CTCCAAGCTT
 721 ATGAAGCGAA GGTTGCAACA GGACAAAGTG TTAATTACAG AGCTCATCCA GCATTCAGCG
 781 AAACATAAGG TTGACATTGA TTGCAGTCAG AAGGTTGTAG TTTACGATCA AAGCTCCCAA
 841 GATGTTGCCT CTCTCTCTTC AGACTGTTTT CTCACTGTAC TTCTGGGTAA ACTGGAGAAG
 901 AGCTTCAACT CTGTTCACCT GCTTGCAGGA GCTGATGCAG CAGAATGGGA TTGGTTATGT
 961 GTTAAATGCC AGCAATACCT GTCCAAAGCC TGACTTTATC CCCGAGTCTC ATTTCCTGCG
1021 TGTGCCTGTG AATGACAGCT TTTGTGAGAA AATTTTGCCG TGGTTGGACA AATCAGTAGA
1081 TTTCATTGAG AAAGCAAAAG CCTCCAATGG ATGTGTTCTA GTGCACTGTT TAGCTGGGAT
1141 CTCCCGCTCC GCCACCATCG CTATCGCCTA CATCATGAAG AGGATGGACA TGTCTTTAGA
1201 TGAAGCTTAC AGATTTGTGA AAGAAAAAAG ACCTACTATA TCTCCAAACT TCAATTTTCT
1261 GGGCCAACTC CTGGACTATG AGAAGAAGAT TAAGAACCAG ACTGGAGCAT CAGGGCCAAA
1321 GAGCAAACTC AAGCTGCTGC ACCTGGAGAA GCCAAATGAA CCTGTCCCTG CTGTCTCAGA
1381 GGGTGGACAG AAAAGCGAGA CGCCCCTCAG TCCACCCTGT GCCGACTCTG CTACCTCAGA
1441 GGCAGCAGGA CAAAGGCCCG TGCATCCCGC CAGCGTGCCC AGCGTGCCCA GCGTGCAGCC
1501 GTCGCTGTTA GAGGACAGCC CGCTGGTACA GGCGCTCAGT GGGCTGCACC TGTCCGCAGA
1561 CAGGCTGGAA GACAGCAATA AGCTCAAGCG TTCCTTCTCT CTGGATATCA AATCAGTTTC
1621 ATATTCAGCC AGCATGGCAG CATCCTTACA TGGCTTCTCC TCATCAGAAG ATGCTTTGGA
1681 ATACTACAAA CCTTCCACTA CTCTGGATGG GACCAACAAG CTATGCCAGT TCTCCCCTGT
1741 TCAGGAACTA TCGGAGCAGA CTCCCGAAAC CAGTCCTGAT AAGGAGGAAG CCAGCATCCC
1801 CAAGAAGCTG CAGACCGCCA GGCCTTCAGA CAGCCAGAGC AAGCGATTGC ATTCGGTCAG
1861 AACCAGCAGC AGTGGCACCG CCCAGAGGTC CCTTTTATCT CCACTGCATC GAAGTGGGAG
1921 CGTGGAGGAC AATTACCACA CCAGCTTCCT TTTCGGCCTT TCCACCAGCC AGCAGCACCT
1981 CACGAAGTCT GCTGGCCTGG GCCTTAAGGG CTGGCACTCG GATATCTTGG CCCCCCAGAC
2041 CTCTACCCCT TCCCTGACCA GCAGCTGGTA TTTTGCCACA GAGTCCTCAC ACTTCTACTC
2101 TGCCTCAGCC ATCTACGGAG GCAGTGCCAG TTACTCTGCC TACAGCTGCA GCCAGCTGCC
2161 CACTTGCGGA GACCAAGTCT ATTCTGTGCG CAGGCGGCAG AAGCCAAGTG ACAGAGCTGA
2221 CTCGCGGCGG AGCTGGCATG AAGAGAGCCC CTTTGAAAAG CAGTTTAAAC GCAGAAGCTG
2281 CCAAATGGAA TTTGGAGAGA GCATCATGTC AGAGAACAGG TCACGGGAAG AGCTGGGGAA
2341 AGTGGGCAGT CAGTCTAGCT TTTCGGGCAG CATGGAAATC ATTGAGGTCT CCTGAGAAGA
2401 AAGACACTTG TGACTTCTAT AGACAATTTT TTTTTCTTGT TCACAAAAAA ATTCCCTGTA
2461 AATCTGAAAT ATATATATGT ACATACATAT ATATTTTTGG AAAATGGAGC TATGGTGTAA
2521 AAGCAACAGG TGGATCAACC CAGTTGTTAC TCTCTTAACA TCTGCATTTG AGAGATCAGC
2581 TAATACTTCT CTCAACAAAA ATGGAAGGGC AGATGCTAGA ATCCCCCCTA GACGGAGGAA
2641 AACCATTTTA TTCAGTGAAT TACACATCCT CTTGTTCTTA AAAAAGCAAG TGTCTTTGGT
2701 GTTGGAGGAC AAAATCCCCT ACCATTTTCC ACGTTGTGCT ACTAAGAGAT CTCAAATATT
2761 AGTCTTTGTC CGGACCCTTC CATAGTACAC CTTAGCGCTG AGACTGAGCC AGCTTGGGGG
2821 TCAGGTAGGT AGACCCTGTT AGGGACAGAG CCTAGTGGTA AATCCAAGAG AAATGATCCT
2881 ATCCAAAGCT GATTCACAAA CCCACGCTCA CCTGACAGCC GAGGGACACG AGCATCACTC
2941 TGCTGGACGG ACCATTAGGG GCCTTGCCAA GGTCTACCTT AGAGCAAACC CAGTACCTCA
3001 GACAGGAAAG TCGGGGCTTT GACCACTACC ATATCTGGTA GCCCATTTTC TAGGCATTGT
3061 GAATAGGTAG GTAGCTAGTC ACACTTTTCA GACCAATTCA AACTGTCTAT GCACAAAATT
3121 CCCGTGGGCC TAGATGGAGA TAATTTTTTT TTCTTCTCAG CTTTATGAAG AGAAGGGAAA
3181 CTGTCTAGGA TTCAGCTGAA CCACCAGGAA CCTGGCAACA TCACGATTTA AGCTAAGGTT
3241 GGGAGGCTAA CGAGTCTACC TCCCTCTTTG TAAATCAAAG AATTGTTTAA AATGGGATTG
3301 TCAATCCTTT AAATAAAGAT GAACTTGGTT TC
```

Figure 4.

MLPLSLQTVFSLYFWVNWRRASTLFTCLQELMQQNGIGYVLNASNTCPKPDFIPESHFLRVPVNDSFCEKILPWLDK
SVDFIEKAKASNGCVLVHCLAGISRSATIAIAYIMKRMDMSLDEAYRFVKEKRPTISPNFNFLGQLLDYEKKIKNQT
GASGPKSKLKLLHLEKPNEPVPAVSEGGQKSETPLSPPCADSATSEAAGQRPVHPASVPSVPSVQPSLLEDSPLVQA
LSGLHLSADRLEDSNKLKRSFSLDIKSVSYSASMAASLHGFSSSEDALEYYKPSTTLDGTNKLCQFSPVQELSEQTP
ETSPDKEEASIPKKLQTARPSDSQSKRLHSVRTSSSGTAQRSLLSPLHRSGSVEDNYHTSFLFGLSTSQQHLTKSAG
LGLKGWHSDILAPQTSTPSLTSSWYFATESSHFYSASAIYGGSASYSAYSCSQLPTCGDQVYSVRRRQKPSDRADSR
RSWHEESPFEKQFKRRSCQMEFGESIMSENRSREELGKVGSQSSFSGSMEIIEVS

Figure 5


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           1        10        20        30        40        50        60        70        80        90
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
    PYST1  DGSPLSNSQPSFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTP-------NLPNLFENAGEFKYKQIPISDHWSQNLSQFFPEAIS
    MKP-7  DGSPVPSSQPAFPVQILPYLYLGCAKDSTNLDVLGKYGIKYILNVTP-------NLPNAFEHGGEFTYKQIPISDHWSQNLSQFFPEAIS
    MKP-4  ATPPPVGLRASFPVQILPNLYLGSARDSANLESLAKLGIRYILNVTP-------NLPNFFEKNGDFHYKQIPISDHWSQNLSRFFPEAIE
     hVH5  LSQPCLPVPSVGLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNASN-------SCPKP-DFICESRFMRVPINDNYCEKLLPWLDKSIE
   DSP-16  ISQPCLPVANIGPTRILPNLYLGCQRDVLNKELMQQNGIGYVLNASN-------TCPKP-DFIPESHFLRVPVNDSFCEKILPWLDKSVD
     PAC1  SDPRVPIYDQGGPVEILPYLYLGSCNHSSDLQGLQACGITAVLNVSA-------SCPNHFE--GLFHYKSIPVEDNQMVEISAWFQEAIS
    MKP-1  SSCSTPLYDQGGPVEILPFLYLGSAYHASRKDMLDALGITALINVSA-------NCPNHFE--GHYQYKSIPVEDNHKADISSWFNEAID
    MKP-2  SSCGTPLHDQGGPVEILPFLYLGSAYHAARRDMLDALGITALLNVSS-------DCPNHFE--GHYQYKCIPVEDNHKADISSWFMEAIE
    MKP-5  NVSYRPAYDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSR-------RTSEACM--THLHYKWIPVEDSHTADISSHFQEAID
      VHR  DGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAAD
Consensus  ...........gpve!lP.lYlGsa........$..lgIt..LNvs........n.pn.fe..g...%k.!p..D.....ls..f.eai.

           91      100       110       120       130       140       150        160 164
           |--------+---------+---------+---------+---------+---------+---------+---|
    PYST1  FIDEA-RGKNCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPNFNFMGQLLDFERTLGLS
    MKP-7  FIDEA-RSKKCGVLVHCLAGISRSVTVTVAYLMQKMNLSLNDAYDFVKRKKSNISPNFNFMGQLLDFERTLGLS
    MKP-4  FIDEA-LSQNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNFNFMGQLLDFERSLRLE
     hVH5  FIDKA-KLSSCQVIVHCLAGISRSATIAIAYIMKTMGMSSDDAYRFVKDRRPSISPNFNFLGQLLEYERTLKLL
   DSP-16  FIEKA-KASNGCVLVHCLAGISRSATIAIAYIMKRMDMSLDEAYRFVKEKRPTISPNFNFLGQLLDYEKKIKNQ
     PAC1  FIDSV-KNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFDFVKQRRGVISPNFSFMGQLLQLETQVLCH
    MKP-1  FIDSI-KNAGGRVFVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAP
    MKP-2  YIDAV-KDCRGRVLVHCQAGISRSATICLAYLMMKKRVRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAT
    MKP-5  FIDCV-REKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRRSMVSPNFGFMGQLLQYESEILPS
      VHR  FIDQALAQKNGRVLVHCREGYSRSPTLVIAYLMMRQKMDVKSALSIVRQNRE-IGPNDGFLAQLCQLNDRLAKE
 Cons n u  FI#.a.....g.VlVHC.aGiSRS.Ti..AYlM......l..A..f!kq.rs.!sPNf.F$gQLl#.#..l...
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